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Assessing Microbial Communities in Transplanted Soils After 21 Years

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Introduction

➢Microbial diversity and community structure are important determinants in biogeochemical cycling and organic matter decomposition.

➢A unique experimental site is located at Agriculture and Agri-Food Canada (AAFC) Research Center in Lethbridge, AB, where diverse soils have been transplanted to one location and managed under common climatic and topographical conditions continuously for >21 years.

➢ Previous analyses have reported a convergence in carbon (C) and nitrogen (N) mineralization rates among transplanted soils. Microbial controls on C and N cycling are well known. We proposed that identical agricultural management practices and common climatic conditions might have the potential to converge microbial community functional groups in these soils over time.

Materials and Methods

Experimental setup

- 36 types of Chernozems were transplanted in 1990 from different locations (Olson et al., 1996).
- Physical, chemical and biological characteristics of transplanted soils varied because of soil origin and agronomic management (Olson et al., 1996).

Split plot design; 3 replicates

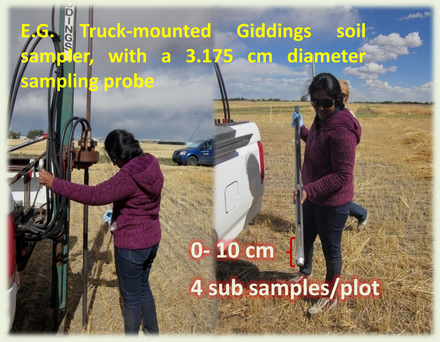
- Main plot factor: transplanted soil type
- Sub plot factor: N rate (0 and 60 kg N ha^{-1})

Treatments for current study: 10 soils were selected (Table 1).

Table 1. Description and background information of selected transplanted soils

Field number	Soil characteristics
2	Native grassland Ah horizon, previously uncultivated soil
4	Continuous dryland wheat since 1911
8	Native grassland (1982) ⟶ cereal production (highest inherent fertility)
9	Native pastureland (highest inherent fertility)
11	Low inherent fertility, Continuous tillage & summer fallow since 1911
16	Irrigated tilled summer fallow since 1911
22	Continuous barley; manure (30 tons ha^{-1} y^{-1}) since 1973
23	Continuous barley ; manure (90 tons ha^{-1} y^{-1}) 1973
26	Native grassland, sub soil from B horizon
27	Native grassland, sub soil from C horizon

Soil Sampling and processing: September 2012



Sieved (4 mm) & stored at -80°C

Freeze dried

Microbial Analysis

Soil Analysis

- Available NO_3^-
- Plant available PO_4^{3-} and K^+
- Available SO_4^{2-}

ALS environmental analytical Lab

Materials and Methods

Phospholipids Fatty acid analysis (PLFA):

Extraction → Phospholipids fatty acid separation solid phase extraction column

19:0 internal std. → Methylation of phospholipids

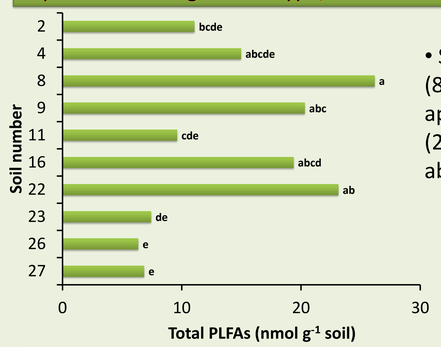
Fatty acid methyl esters → Hewlett-Packard 5890 Series II gas chromatograph (J&W Scientific)

Statistical analysis

- Analysis of variance ANOVA (a = 0.05) – PLFA & soil chemical properties
- Means were separated by LSD

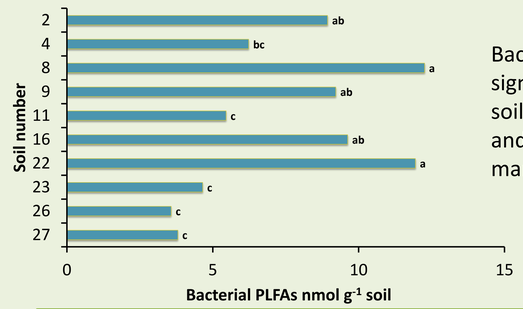
Results & Discussion

After 21 years, microbial biomass dynamics in diverse transplanted soils were dependent on original soil type, but not N fertilizer.



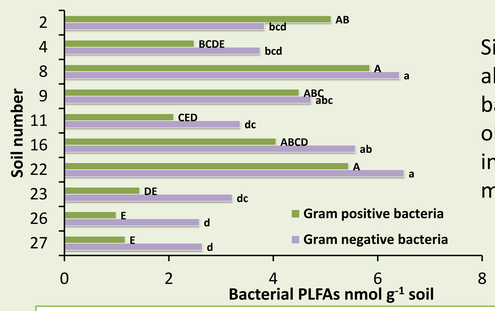
- Soils with highest inherent fertility (8,9) and a history of manure application at recommended rate (22), had the highest microbial abundance.

Fig.1 Total microbial biomass measured in transplanted soil



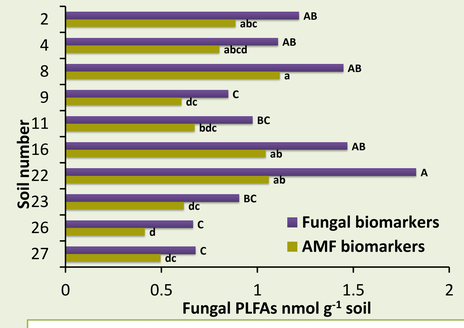
Bacterial abundance was significantly ($p<0.001$) lower in soils with low inherent fertility and a history of excessive manure application

Fig.4 Bacterial abundance



Similar to total bacterial abundance, lowest G^+ and G^- bacterial abundance was observed in soils with low inherent fertility and excessive manure application.

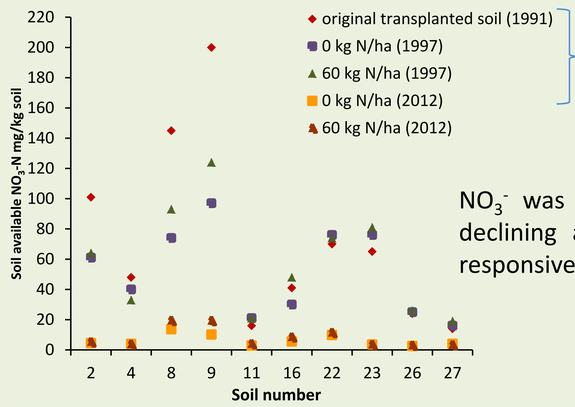
Fig.3 G^+ and G^- bacterial abundance



Two levels (high and low) of distribution for fungal and AMF biomarkers were observed among soil types.

Fig.2 Fungal and AMF abundance

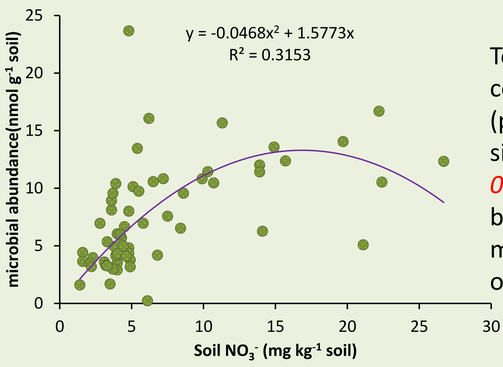
Results and Discussion



NO_3^- was variable over time declining and becoming less responsive to N application

Fig. 5: Available soil nitrate in 1991, 1997 and 2012

Available NO_3^- and SO_4^{2-} were affected by both soil type and N rate ($p<0.05$). Soil available K^+ and PO_4^{3-} were significantly varied in transplanted soils; high in manured and previously uncultivated soils (22, 16) (data not presented).



Total PLFA was positively correlated with soil NO_3^- ($p<0.001$). There was a significant quadratic *($p < 0.017$)* relationship between total PLFA and the model accounted for 31 % of variation.

Fig.6 Relationship between soil NO_3^- and microbial abundance

- Microbial biomass, fungal and bacterial biomarkers varied among soils, dividing soils into two distinct groups with similar characters. Soils with higher fertility by inherent or manure application are rich in microbial abundance. However, application of excessive amount of manure exhibit very low microbial profiles.
- In agreement with Zvoumya et al (2008) the current study also observed a trend of convergence in mineral N.

Conclusion and Future work

PLFA profiling of transplanted soils after 21 years indicated that initial conditions have dominant impact on abundance and community composition of soil microbes even after decades under identical conditions.

Further investigation will be conducted by evaluating 16S rRNA from 1991 & 2011 archived soils to see degree of microbial convergence over time. ^{13}C labelled Incubation study will be conducted to observe the behavior of active C assimilation.

References

- Olson, B. M., H. H. Janazen, F. J. Larney, and L. J. Selinger.1996. A proposed method for measuring the effect of soil quality on productivity.Agronomy Journal.88: 497-500.
- Zvomuya, F., H. H. Janzen and F. J. Larney.2008.A Long-Term Field Bioassay of Soil QualityIndicators in a Semiarid Environment.Soil Science Society of America

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